

Extension-Trapping SNP Assay

Highly stringent annealing conditions (gDNA is biotinylated prior to assay):

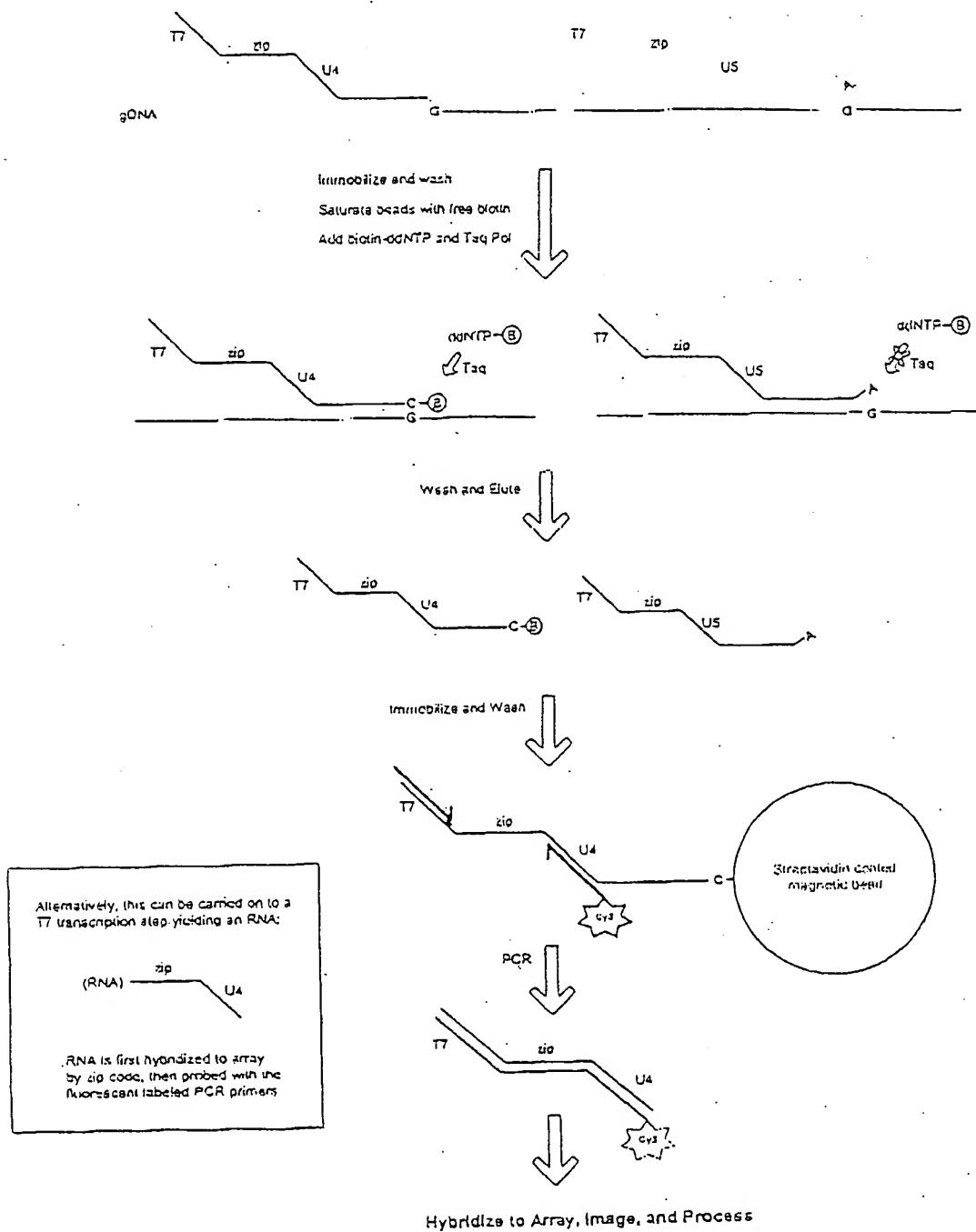


FIGURE 1

## Reduced Genome Single Base Extension Assay:

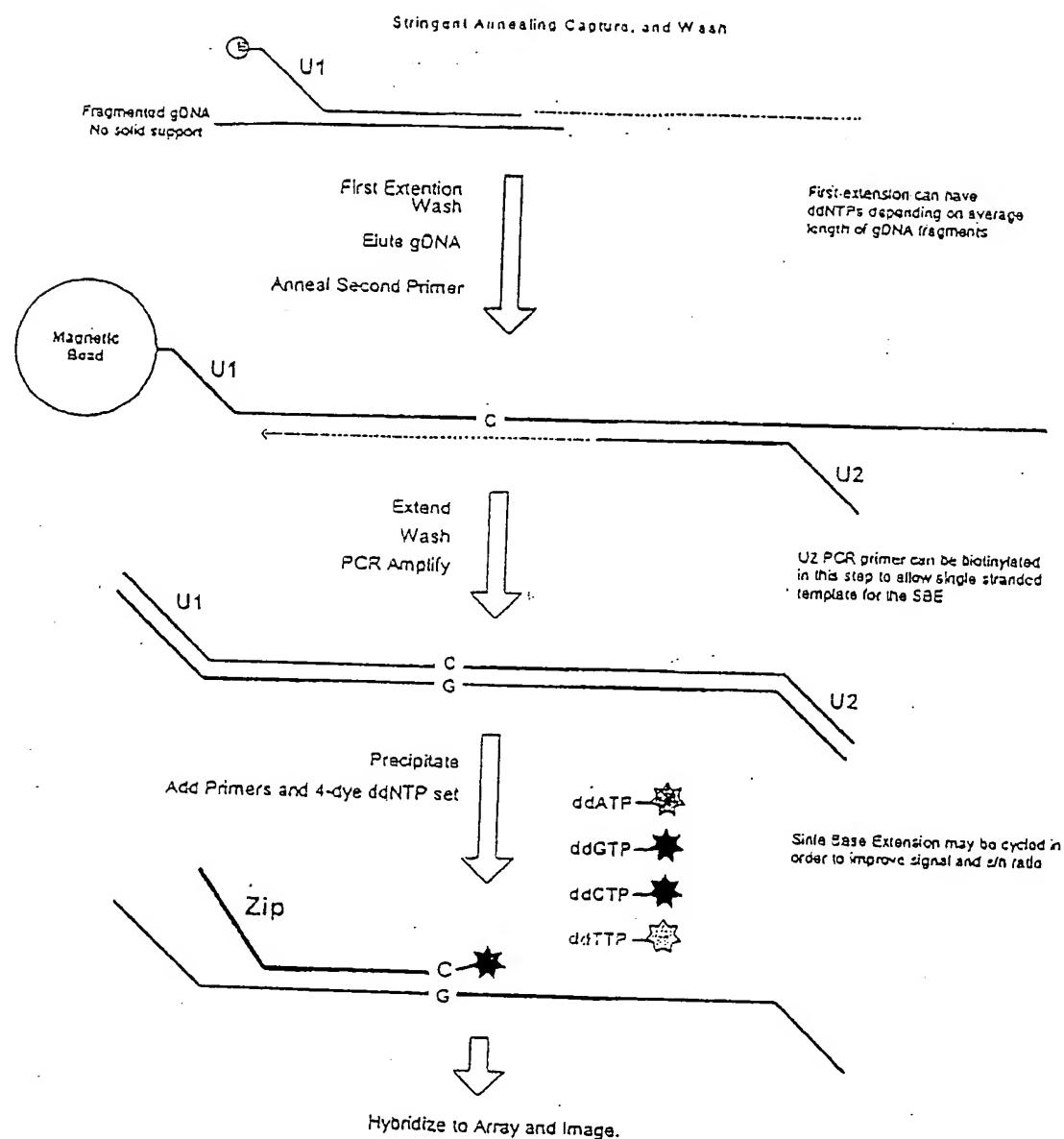


FIGURE 2

## Complexity Reduction and Multiplex Assay

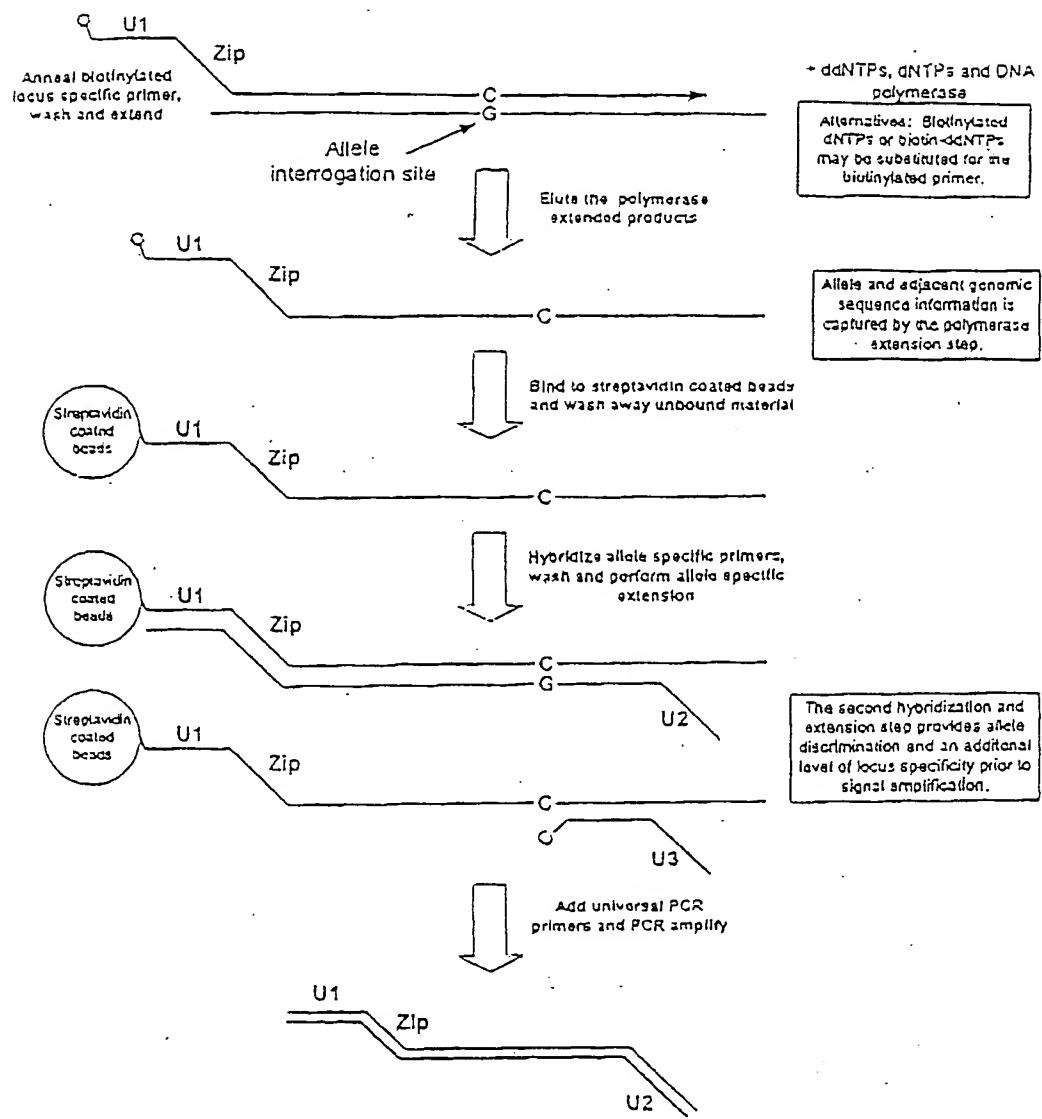


FIGURE 3

## Complexity Reduction and Multiplex Assay

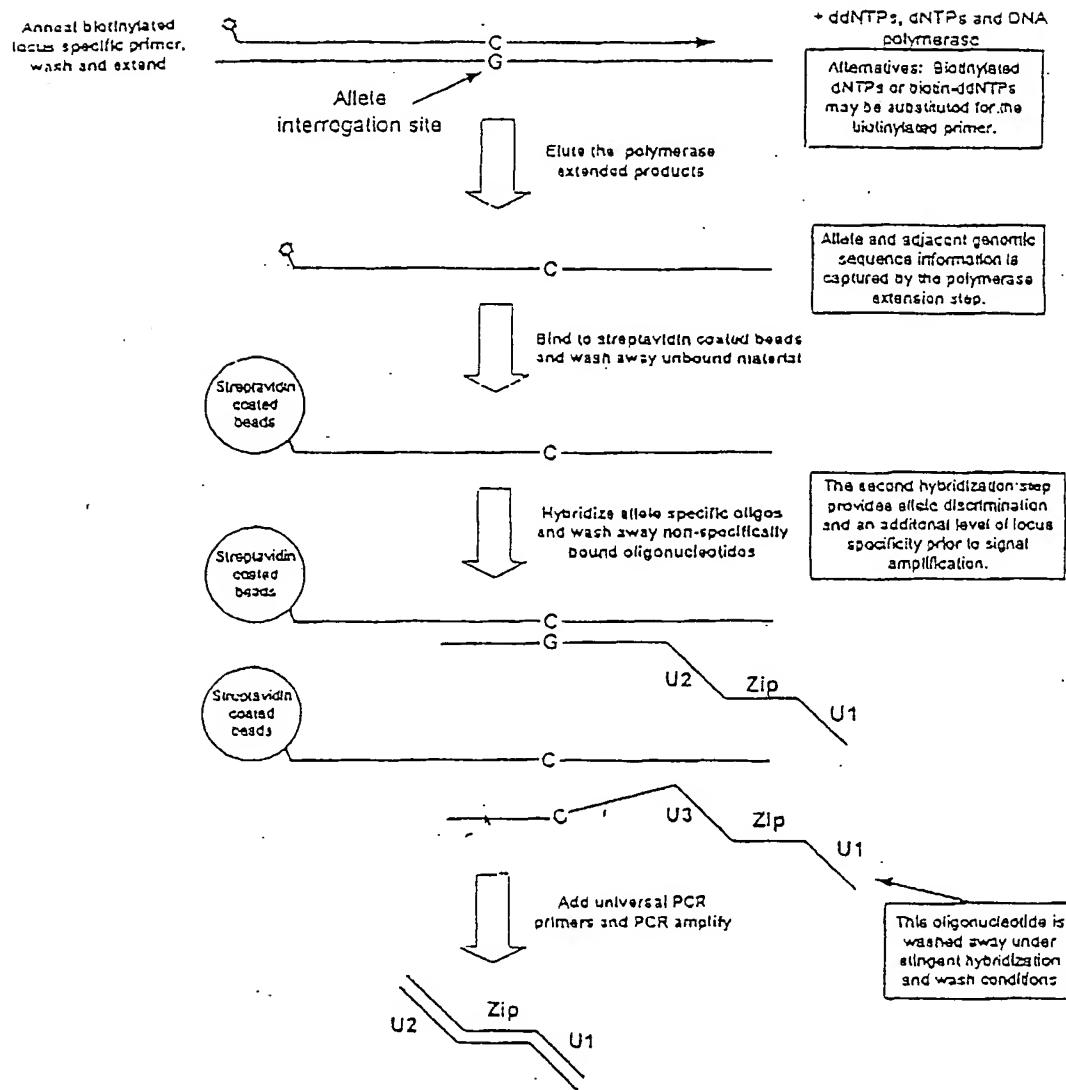


FIGURE 4

### Complexity reduction and multiplex Assay

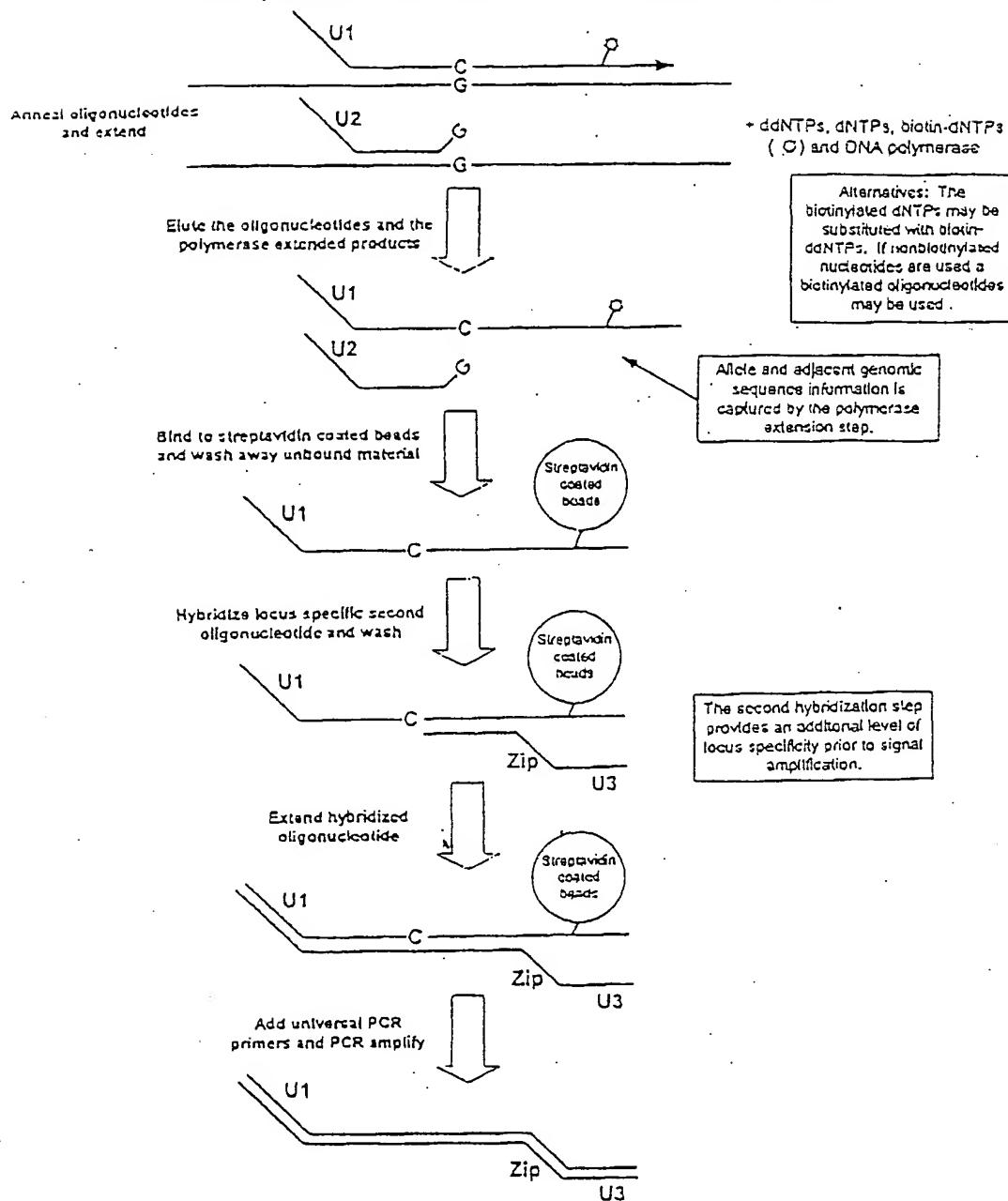


FIGURE 5

## Complexity Reduction and Multiplex Assay

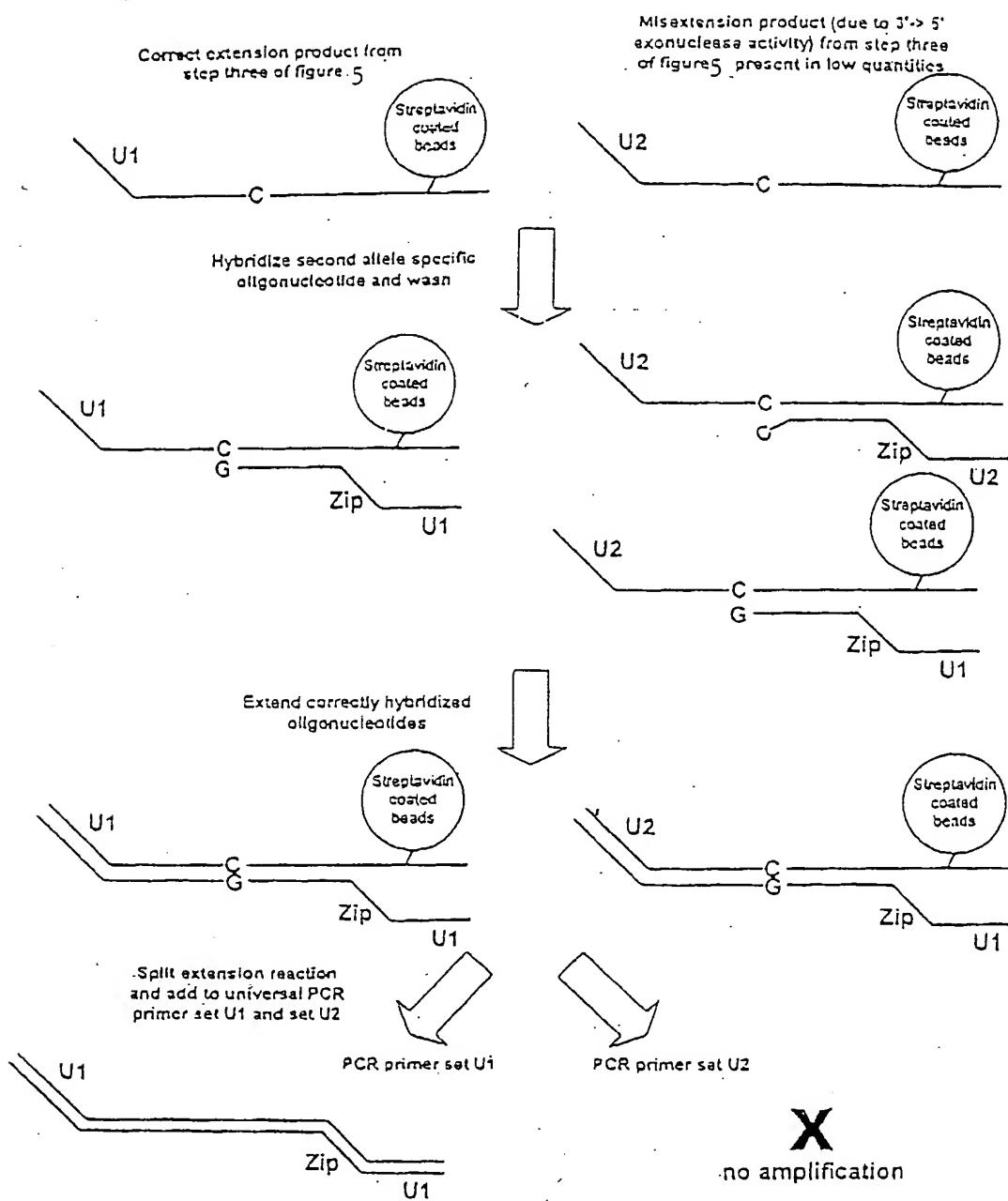
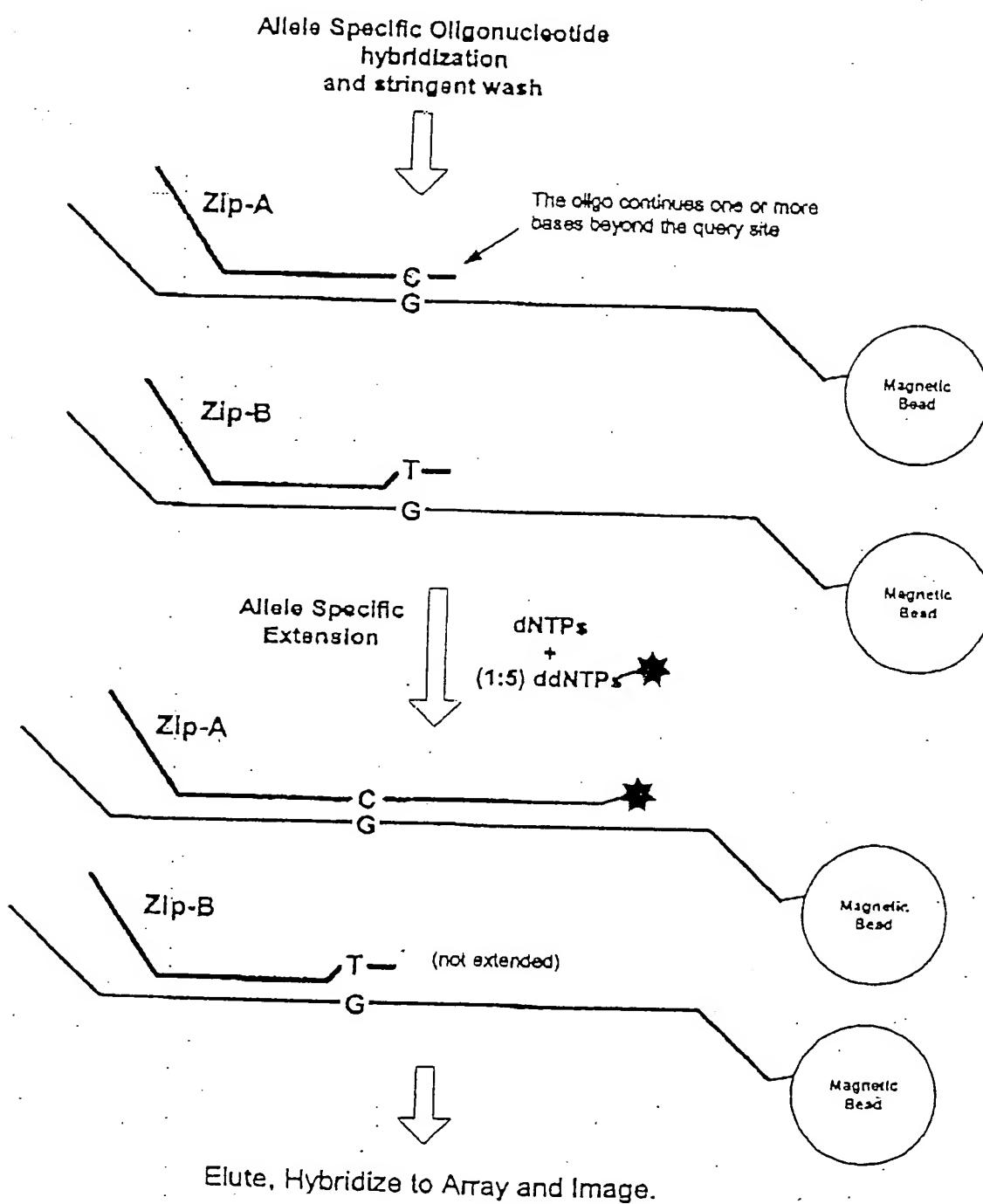


FIGURE 6

### Solid Phase Locus-Specific Primer Extension

Starting material is immobilized, single stranded universal PCR product. There are several ways to generate this.



Alternate labeling scheme for primer extension (high signal)

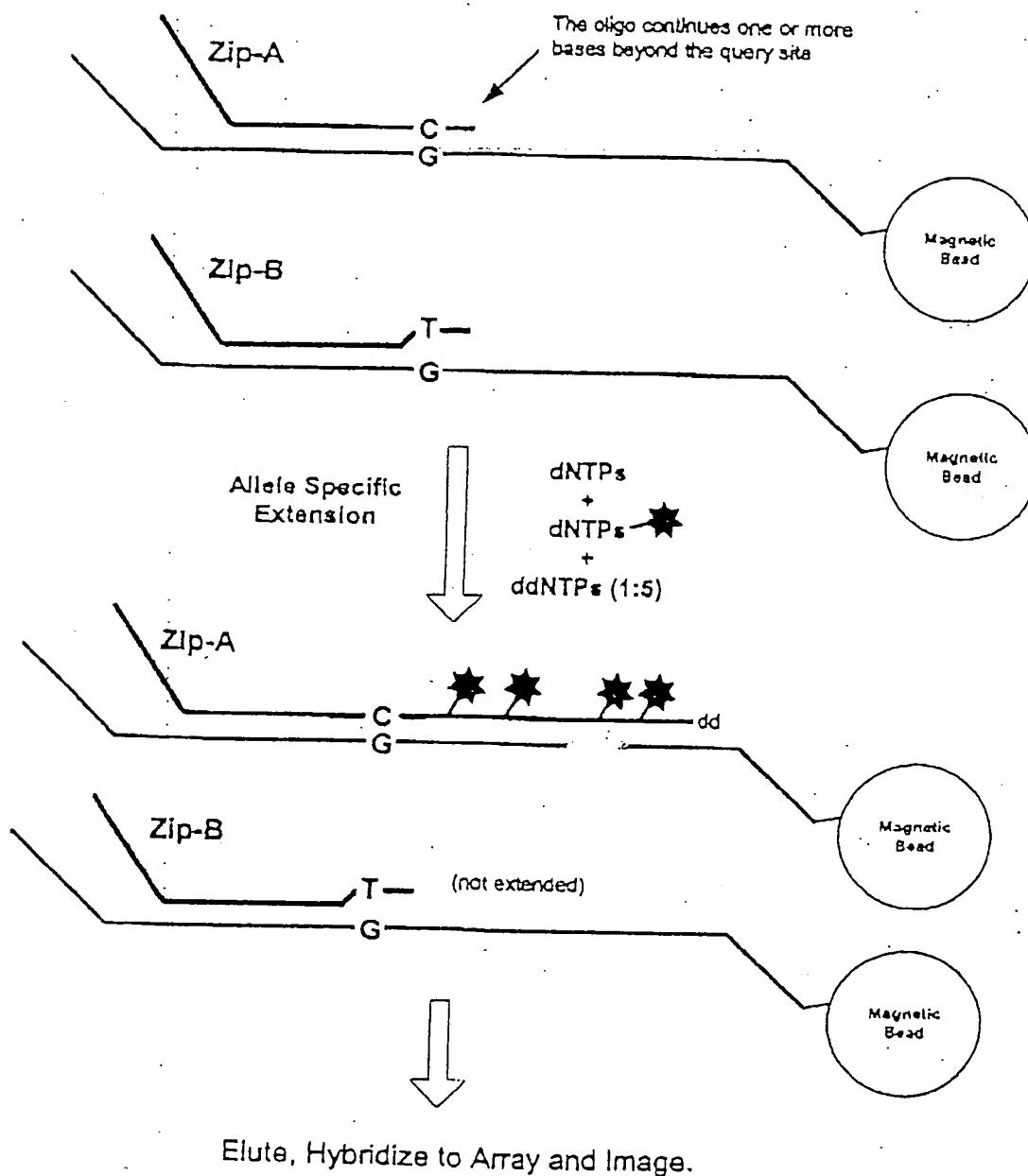


FIGURE 8

## Simplified QLA-PCR Assay Format

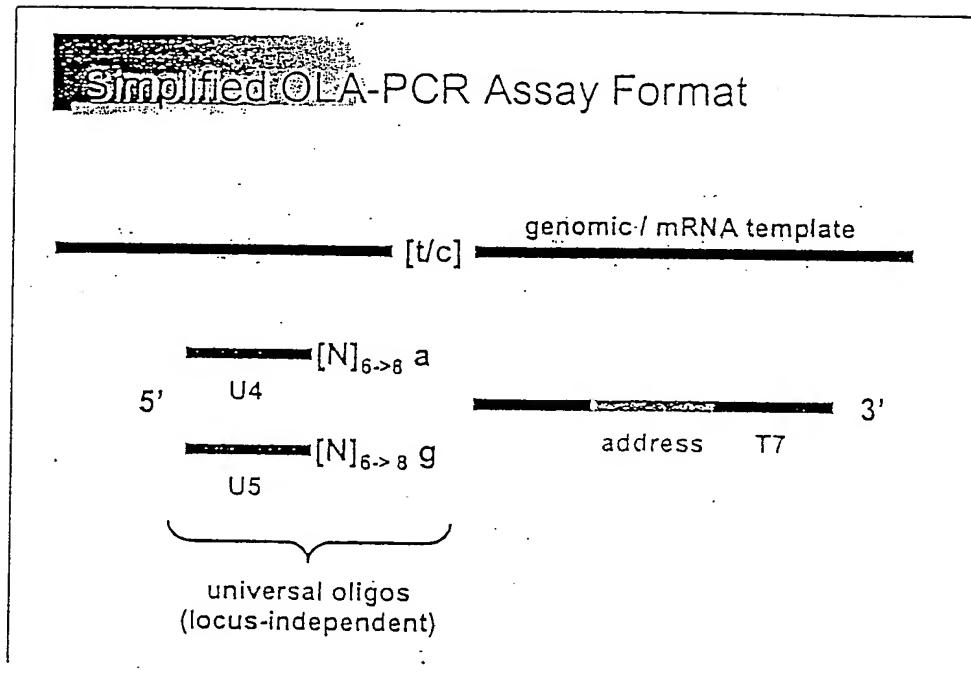


FIGURE 9

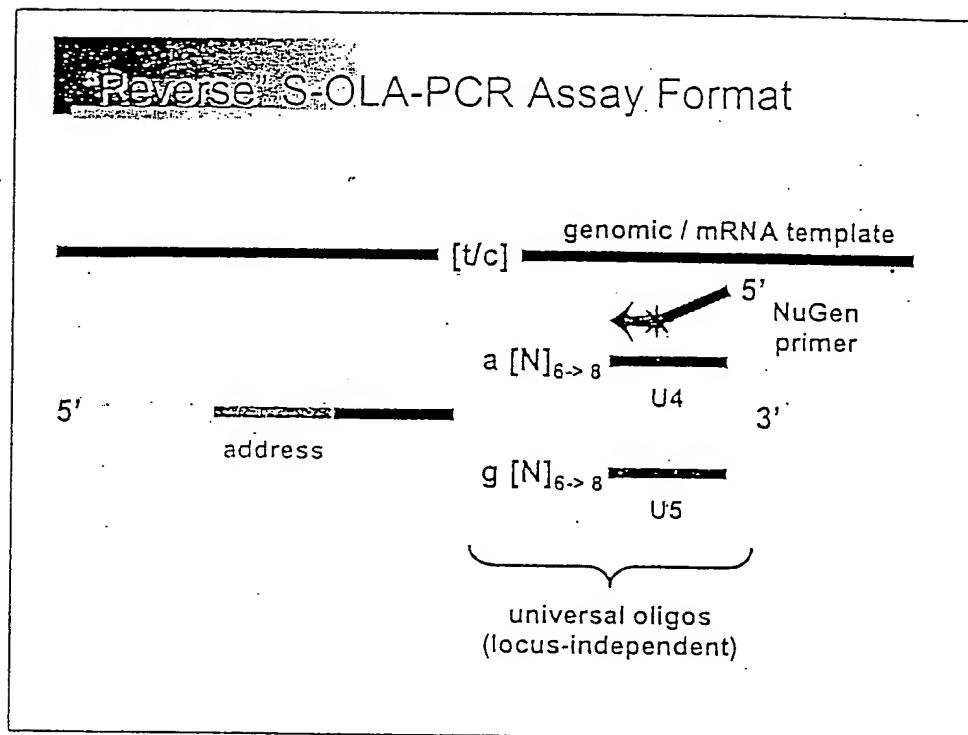


FIGURE 10

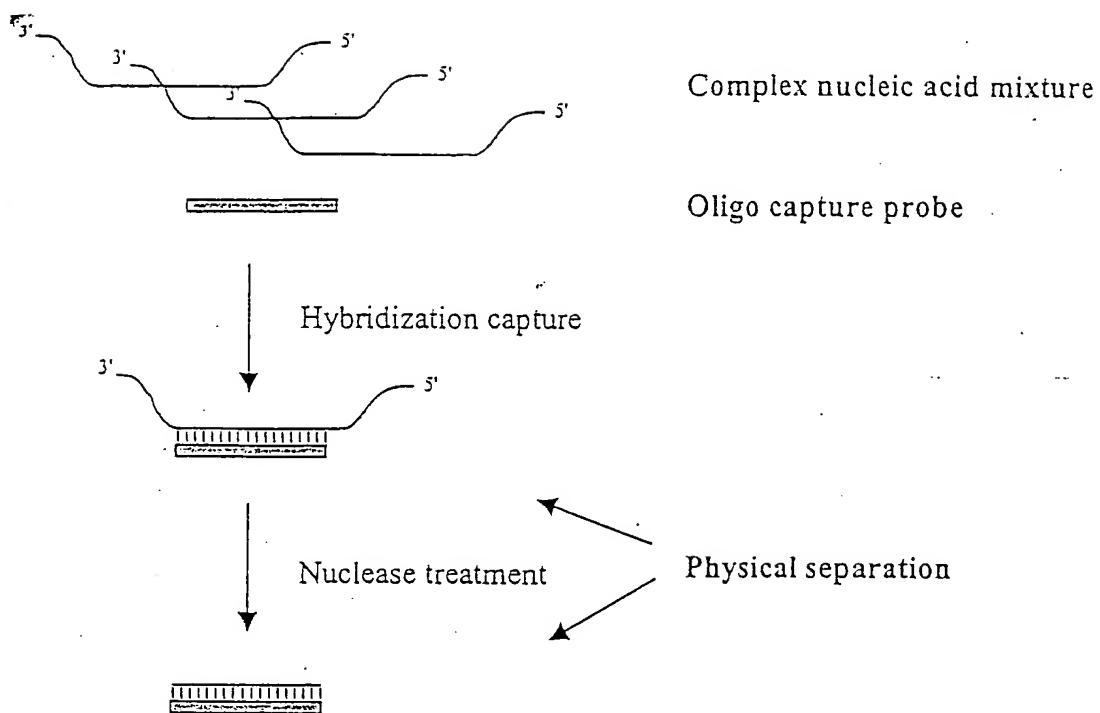


FIGURE 11

Principle of ICAN method

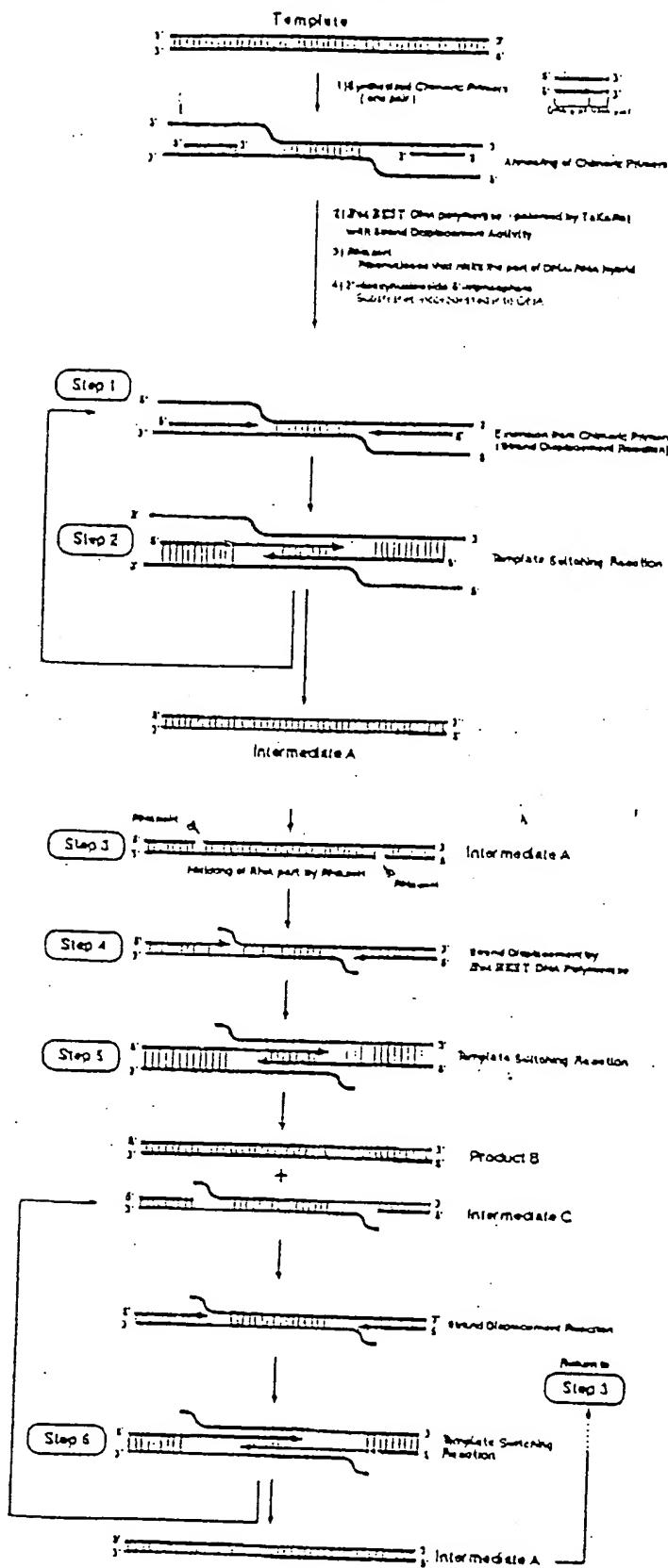


FIGURE 12

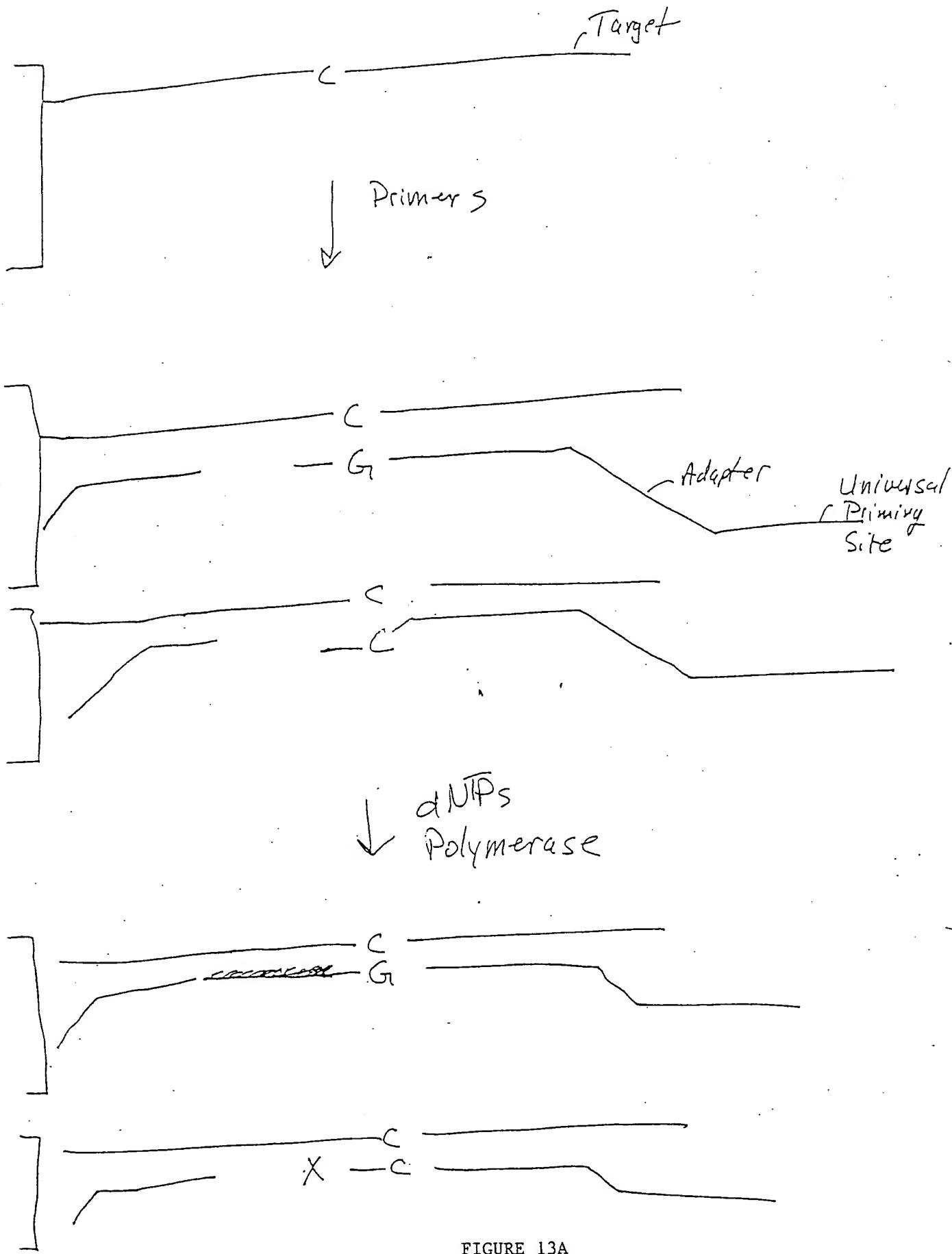
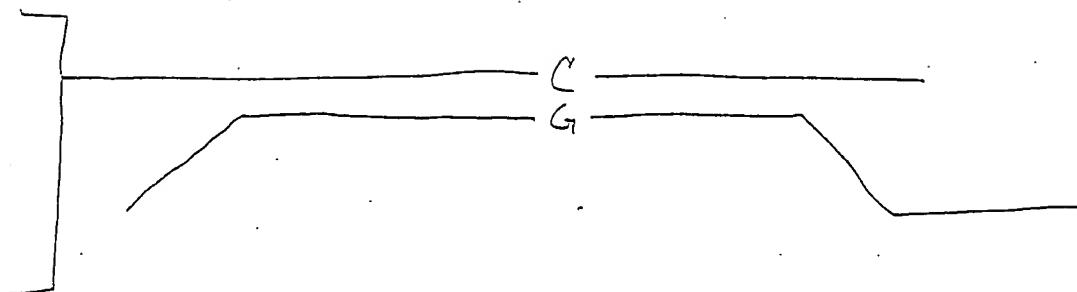
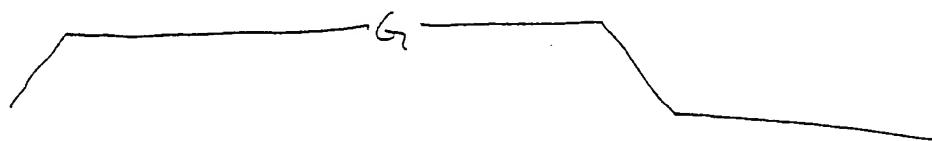


FIGURE 13A

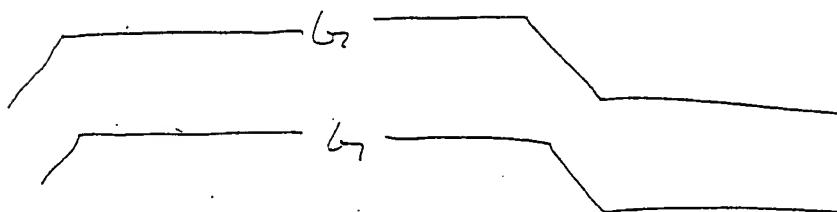
↓ Ligase



↓ Denature



↓ + Primers  
+ dNTP\*  
+ Amplification Enzyme



↓

↓ Detect

FIGURE 13B

# SNP Genotyping: 1152 Multiplex; 96 DNAs

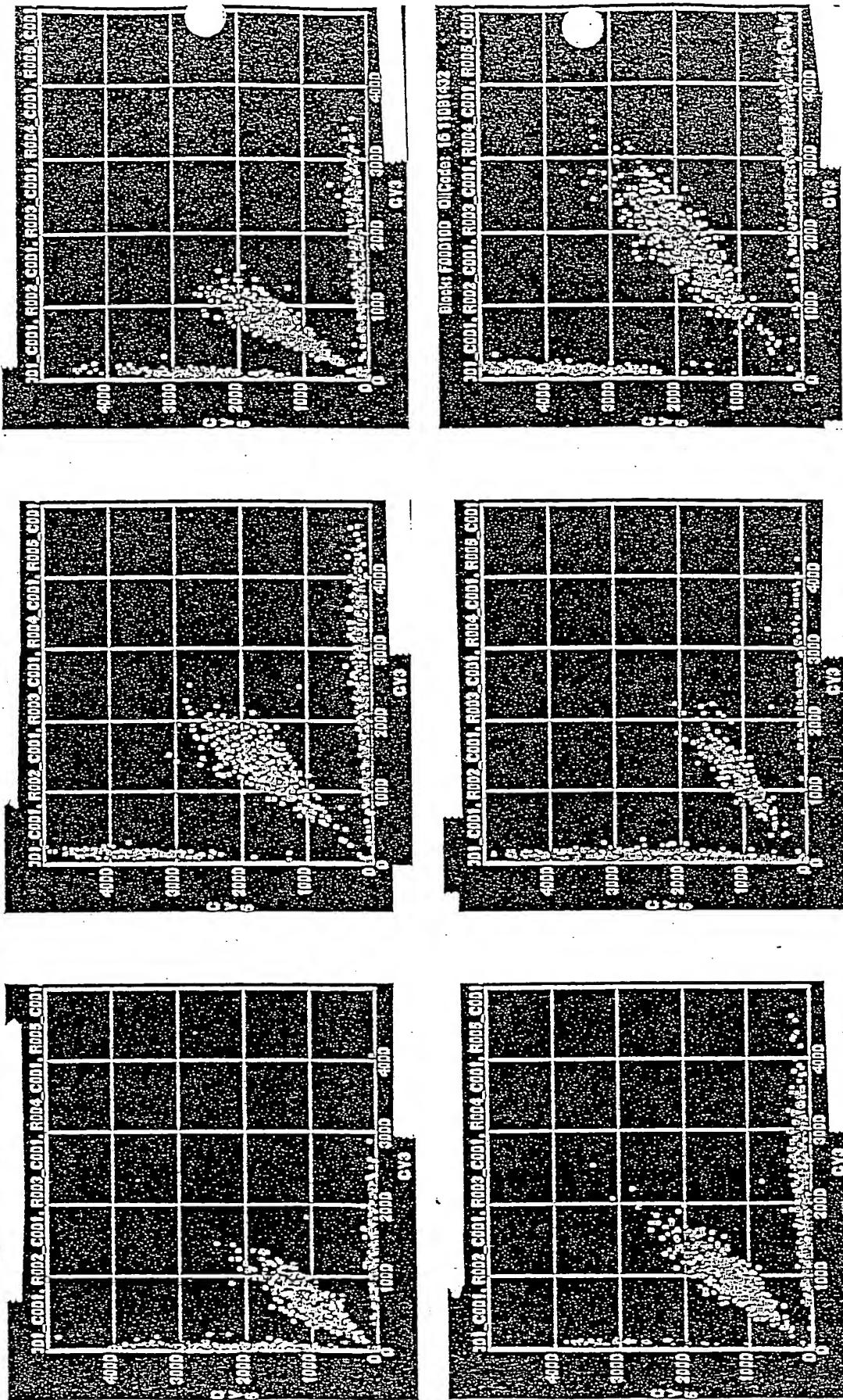


FIGURE 14

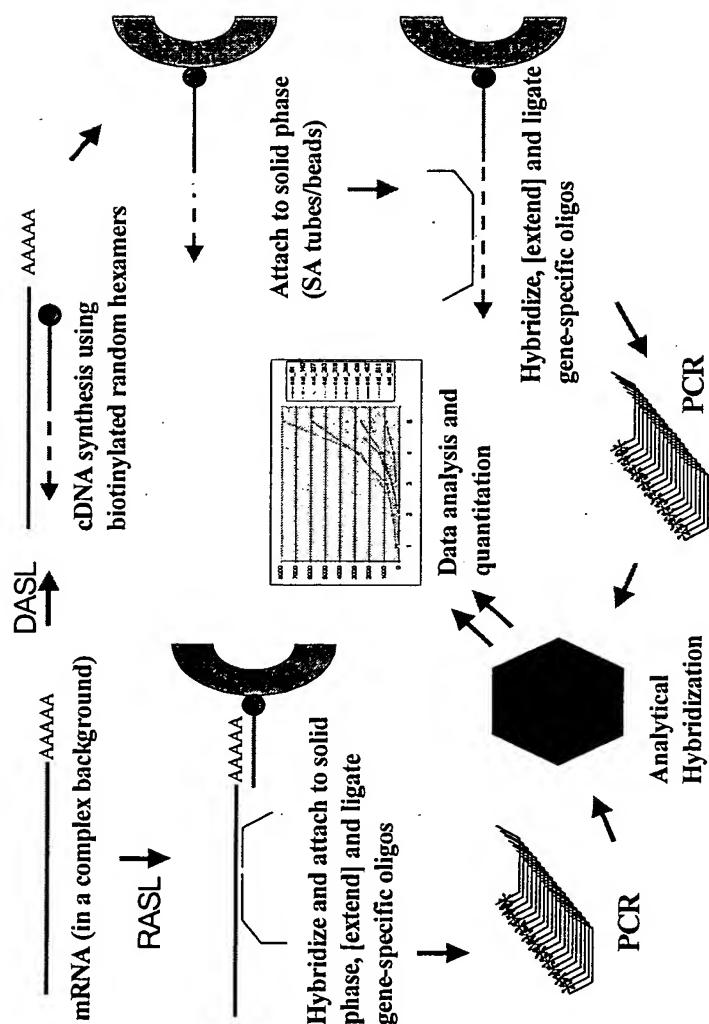


FIGURE 15

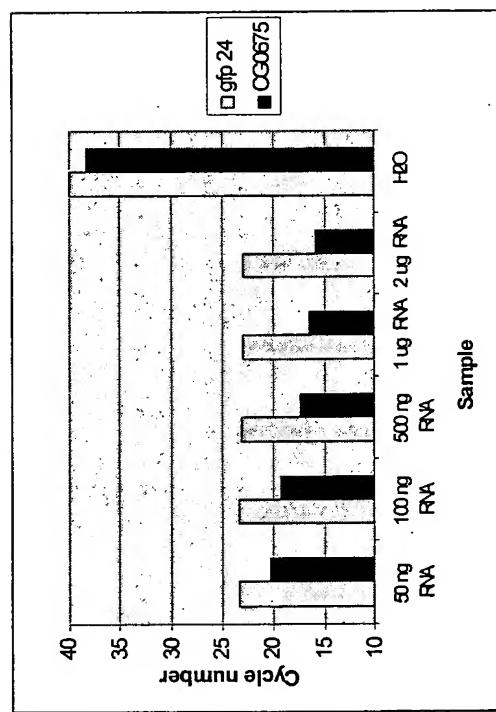
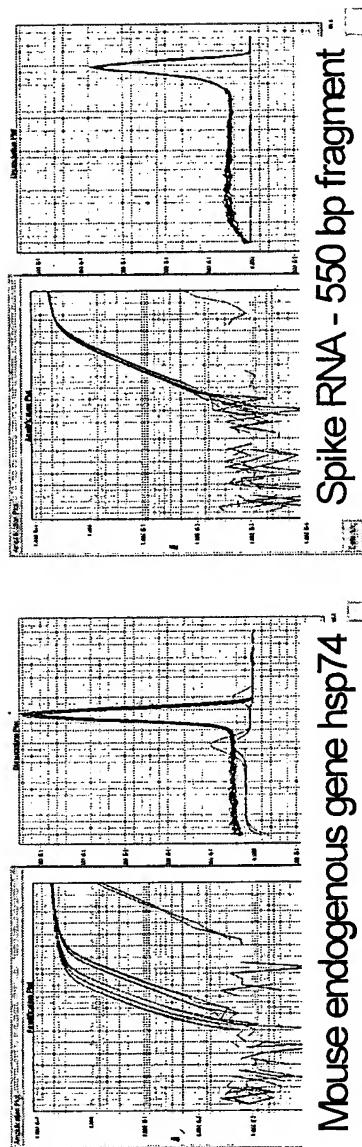
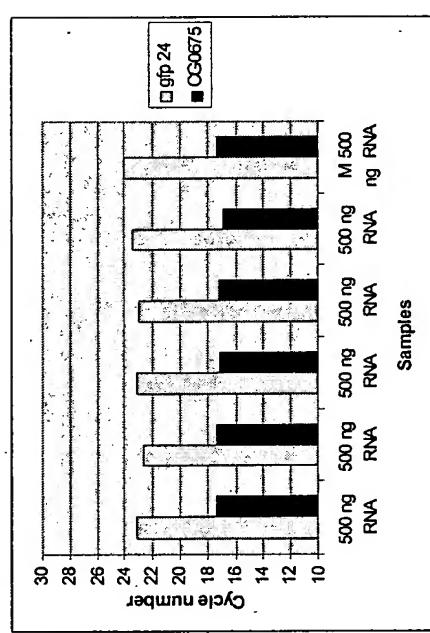
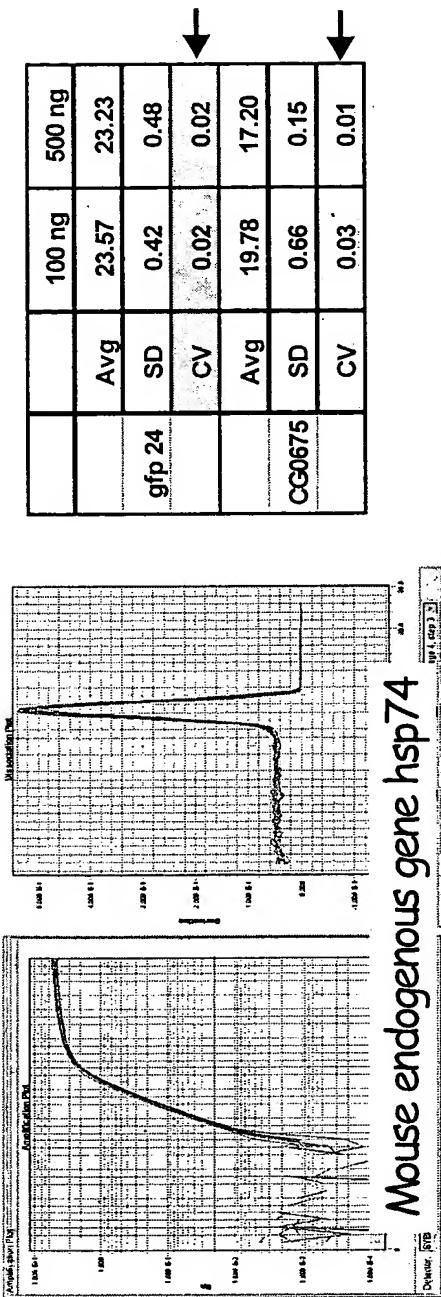


FIGURE 16



● cDNA synthesis on the robot was reproducible and as good as in the manual reaction (at least for the tested genes).

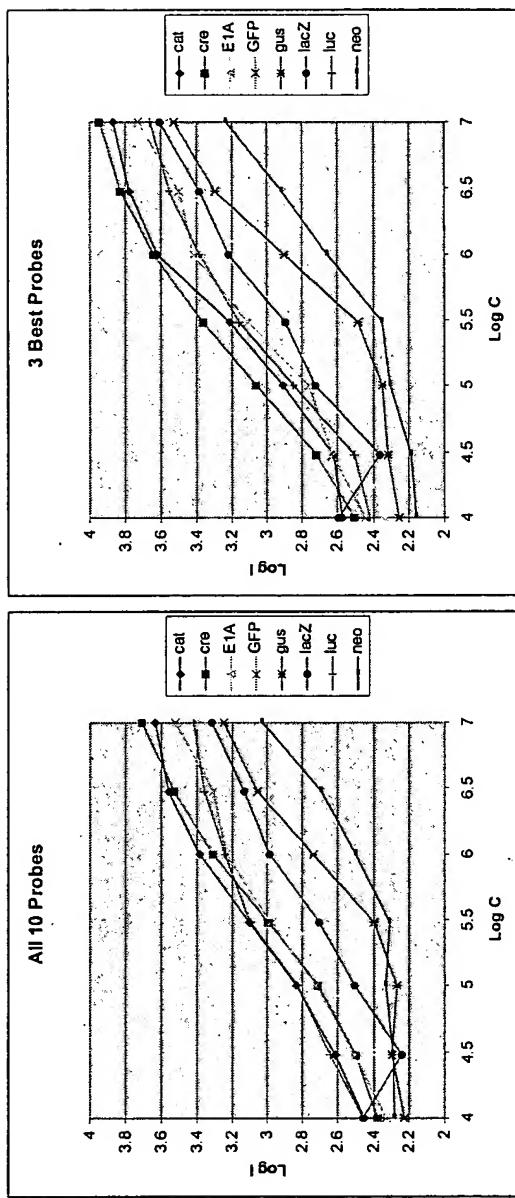
FIGURE 17

|      | pool 1   | pool 2   | pool 3   | pool 4   | pool 5   | pool 6   | pool 7   | pool 8   |
|------|----------|----------|----------|----------|----------|----------|----------|----------|
| cat  | 0.00E+00 | 1.00E+04 | 3.00E+04 | 1.00E+05 | 3.00E+05 | 1.00E+06 | 3.00E+06 | 1.00E+07 |
| cre  | 1.00E+04 | 3.00E+04 | 1.00E+05 | 3.00E+05 | 1.00E+06 | 3.00E+06 | 1.00E+07 | 0.00E+00 |
| E1A  | 3.00E+04 | 1.00E+05 | 3.00E+05 | 1.00E+06 | 3.00E+06 | 1.00E+07 | 0.00E+00 | 1.00E+04 |
| GFP  | 1.00E+05 | 3.00E+05 | 1.00E+06 | 3.00E+06 | 1.00E+07 | 0.00E+00 | 1.00E+04 | 3.00E+04 |
| gus  | 3.00E+05 | 1.00E+06 | 3.00E+06 | 1.00E+07 | 0.00E+00 | 1.00E+04 | 3.00E+04 | 1.00E+05 |
| lacZ | 1.00E+06 | 3.00E+06 | 1.00E+07 | 0.00E+00 | 1.00E+04 | 3.00E+04 | 1.00E+05 | 3.00E+05 |
| luc  | 3.00E+06 | 1.00E+07 | 0.00E+00 | 1.00E+04 | 3.00E+04 | 1.00E+05 | 3.00E+05 | 1.00E+06 |
| neo  | 1.00E+07 | 0.00E+00 | 1.00E+04 | 3.00E+04 | 1.00E+05 | 3.00E+05 | 1.00E+06 | 3.00E+06 |
| bla  | 3.00E+05 |
| GST  | 3.00E+05 |



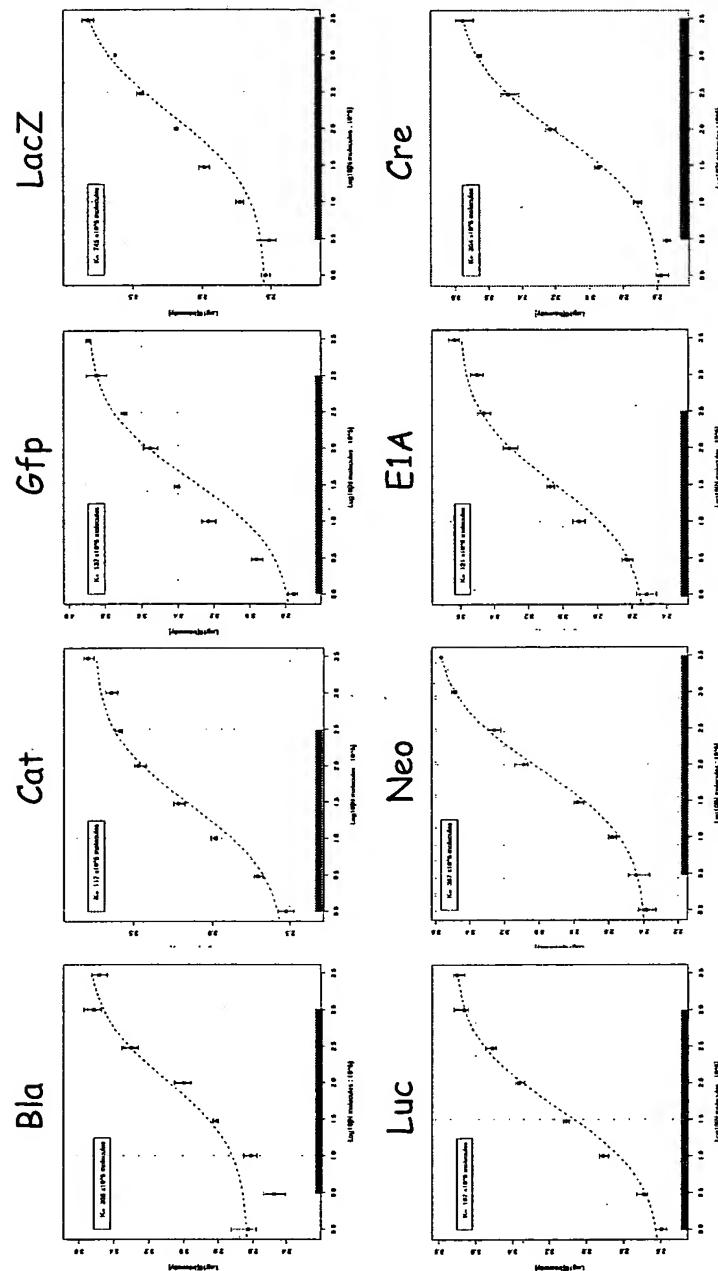
FIGURE 18

Selecting 3 probes that perform well gives better data than averaging all probes.



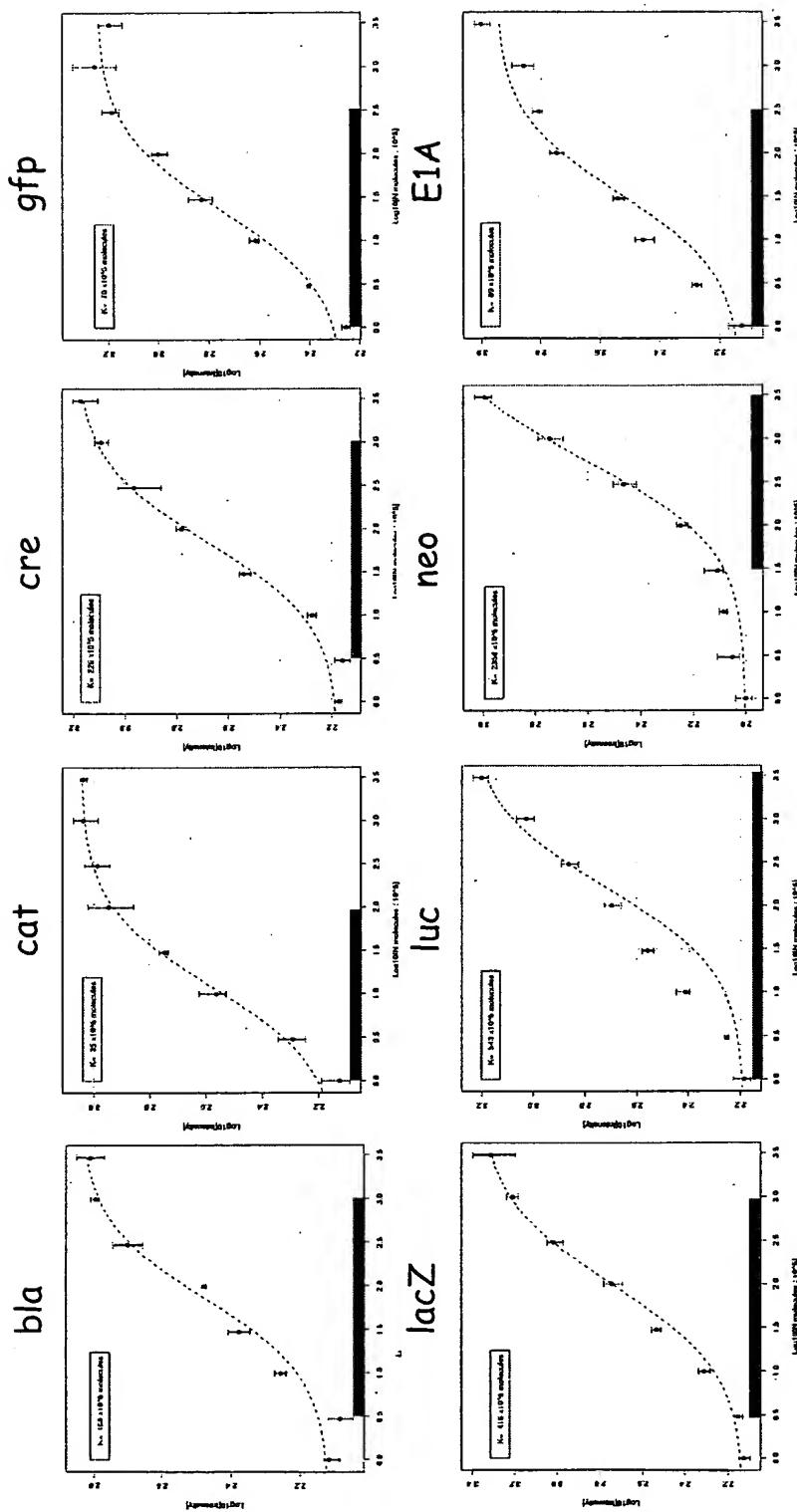
Matrix 4, 238-plex, 100 ng total RNA background

FIGURE 19



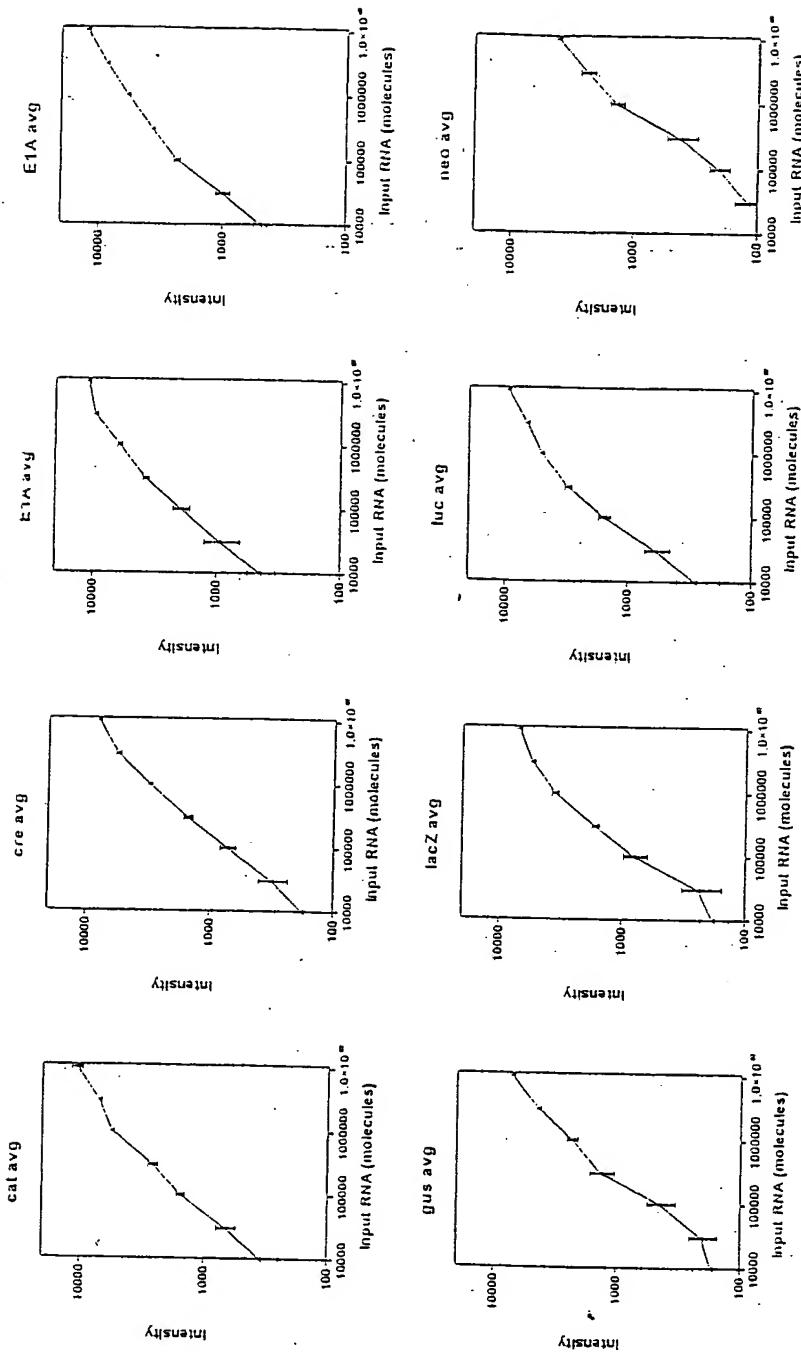
- 3 fold detection range
- Error bars represent the range of intensities of 4 replicates.

FIGURE 20



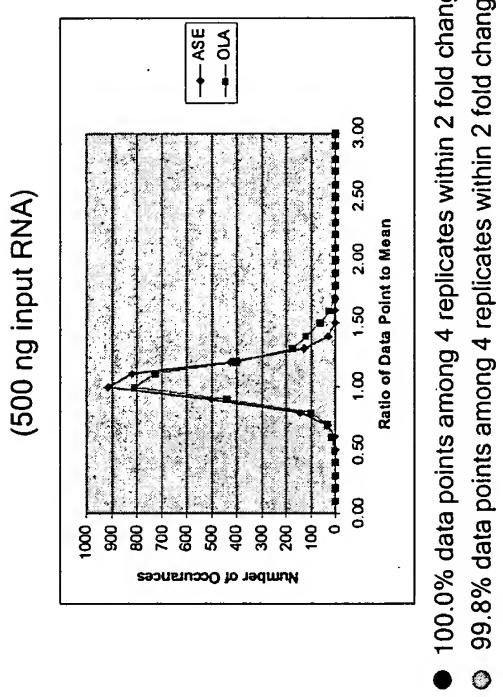
250 ng of total RNA / sample  
Ds DNA hybridization  
Error bars represent the range of intensities of 4 replicates.

FIGURE 21



# 100 ng total RNA background, 12 replicates, 238-plex.  
 # all pre-PCR and post-PCR processes identical to SciOps  
 # including single stranded product hybridization to arrays.  
 # Dynamic range: 2.5 - 3 logs; Precision: better than 3 fold change.

FIGURE 22



- 100.0% data points among 4 replicates within 2 fold change
- 99.8% data points among 4 replicates within 2 fold change

FIGURE 23

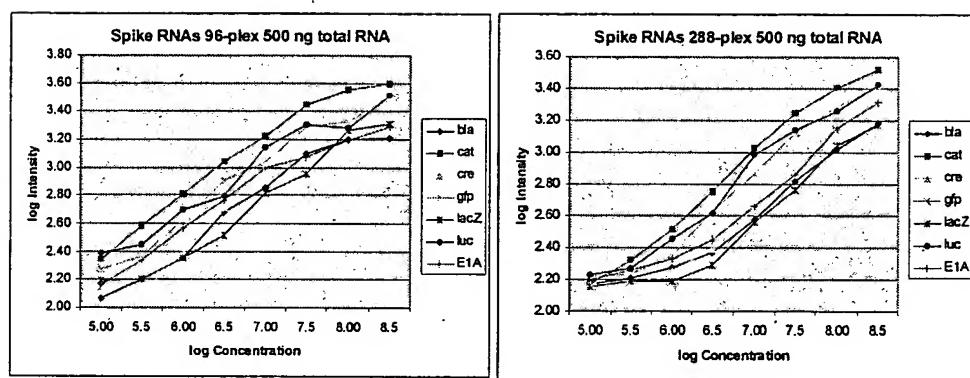


FIGURE 24

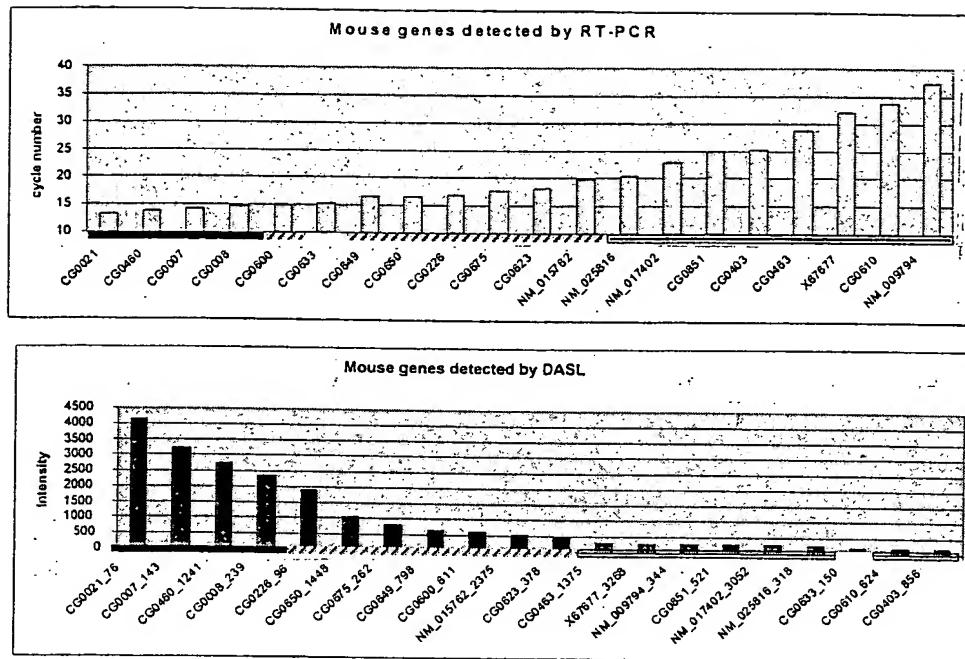


FIGURE 25

# How to Handle Genes Expressed at Different Levels?

Title: Multiplex Nucleic Acid Reactions  
Inventors: Chee et al.  
Filing Date: Herewith  
Attorney Client-Matter No.: 67234-015  
(858-535-9001)

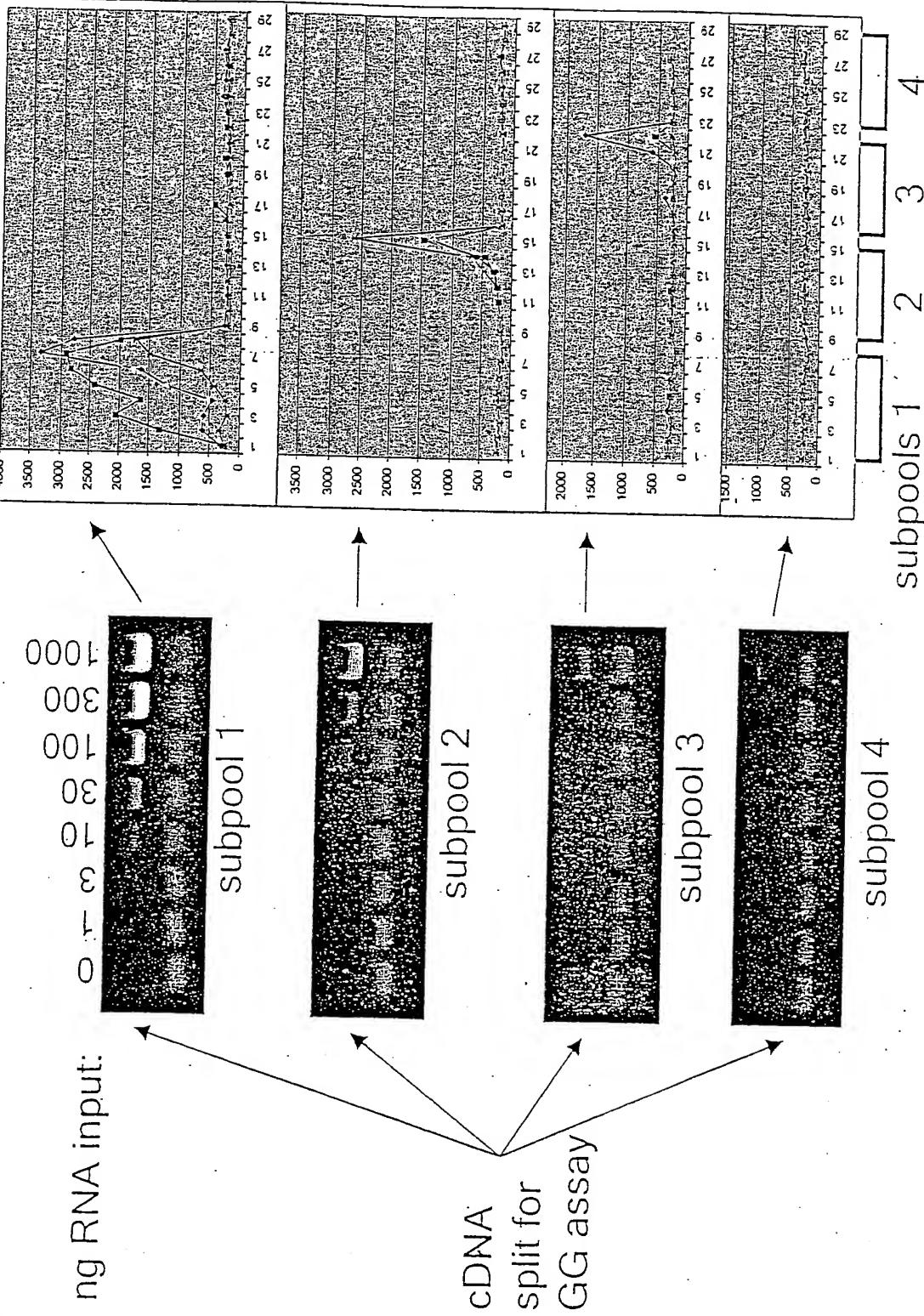


FIGURE 26

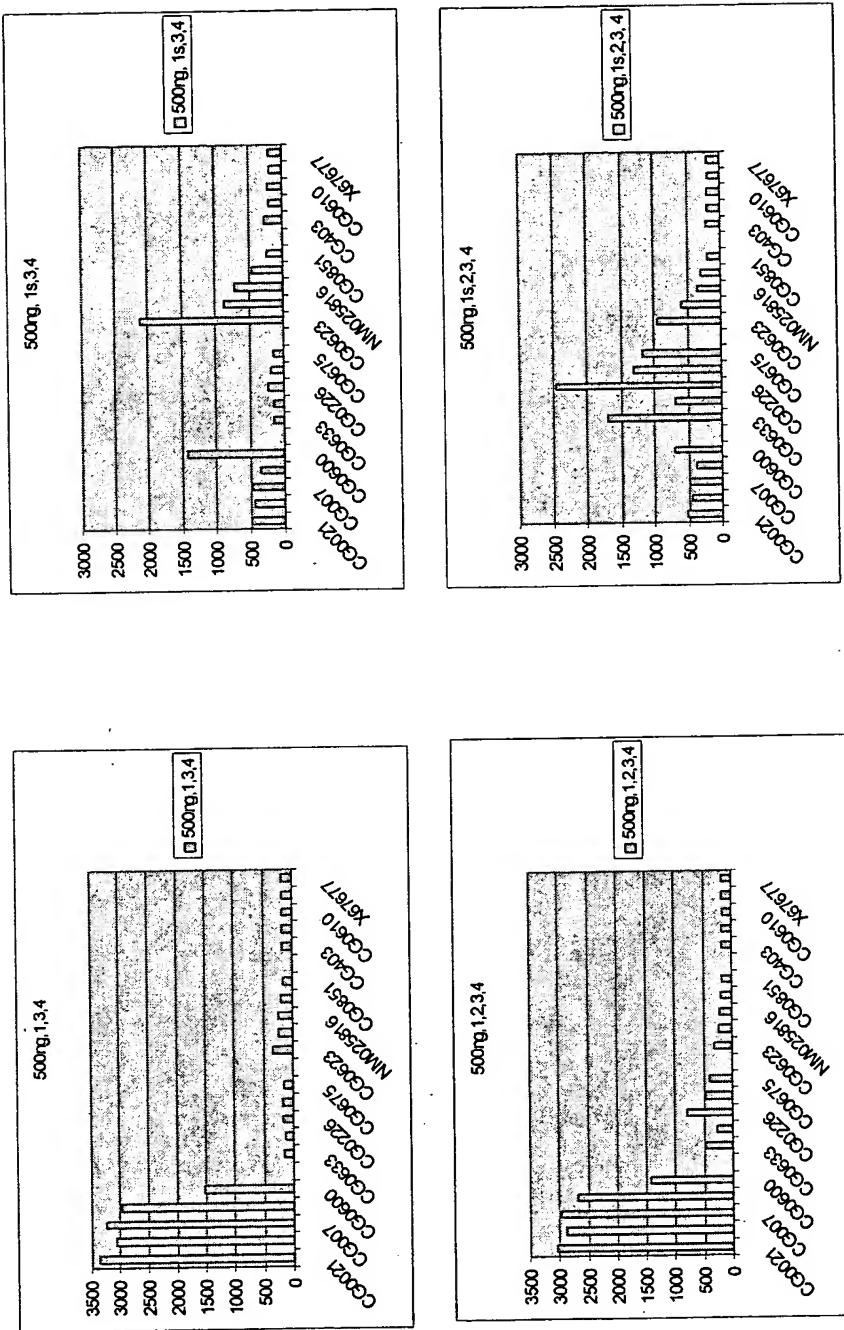


FIGURE 27